

SEQUENCE LISTING

<110> Rory A.J. Curtis

<120> 55053, A Novel Human Eukaryotic Kinase
and Uses Therefor

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Gln His Ala Gln Tyr Val Gly Pro Tyr Arg Leu Glu Lys Thr Leu Gly
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Lys Gly Gln Thr Gly Leu Val Lys Leu Gly Val His Cys Ile Thr Gly
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Gln Lys Val Ala Ile Lys Ile Val Asn Arg Glu Lys Leu Ser Glu Ser
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Val Leu Met Lys Val Glu Arg Glu Ile Ala Ile Leu Lys Leu Ile Glu
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His Pro His Val Leu Lys Leu His Asp Val Tyr Glu Asn Lys Lys Tyr
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Pro	Ser	Pro	Gly	Gly	Gly	Val	Gly	Gly	Ala	Ala	Trp	Arg	Ser	Arg	Leu		
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35 40 45
Lys Leu Gly Val His Cys Ile Thr Gly Gln Lys Val Ala Ile Lys Ile
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Val Asn Arg Glu Lys Leu Ser Glu Ser Val Leu Met Lys Val Glu Arg
65 70 75 80
Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro His Val Leu Lys Leu
85 90 95
His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr Leu Val Leu Glu His
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Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val Lys Lys Gly Arg Leu
115 120 125
Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln Ile Val Ser Ala Leu
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Asp Phe Cys His Ser Tyr Ser Ile Cys His Arg Asp Leu Lys Pro Glu
145 150 155 160
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Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly
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Ser Pro His Tyr Ala Cys Pro Glu Val Ile Lys Gly Glu Lys Tyr Asp
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Gly Arg Arg Ala Asp Met Trp Ser Cys Gly Val Ile Leu Phe Ala Leu
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Leu Val Gly Ala Leu Pro Phe Asp Asp Asp Asn Leu Arg Gln Leu Leu
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Glu Lys Val Lys Arg Gly Val Phe His Met Pro His Phe Ile Pro Pro
245 250 255
Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu Val Glu Pro Glu Lys
260 265 270
Arg Leu Ser Leu Glu Gln Ile Gln Lys His Pro Trp Tyr Leu Gly Gly
275 280 285
Lys His Glu Pro Asp Pro Cys Leu Glu Pro Ala Pro Gly Arg Arg Val
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Ala Met Arg Ser Leu Pro Ser Asn Gly Glu Leu Asp Pro Asp Val Leu
305 310 315 320
Glu Ser Met Ala Ser Leu Gly Cys Phe Arg Asp Arg Glu Arg Leu His
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Arg Glu Leu Arg Ser Glu Glu Glu Asn Gln Glu Lys Met Ile Tyr Tyr
340 345 350
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Pro Met Leu Ser Arg His Gly Lys Arg Arg Pro Glu Arg Lys Ser Met
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Glu Val Leu Ser Ile Thr Asp Ala Gly Gly Gly Ser Pro Val Pro
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Thr Arg Arg Ala Leu Glu Met Ala Gln His Ser Gln Arg Ser Arg Ser
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 485 490 495
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 Arg Ser Trp Phe Gly Asn Phe Ile Ser Leu Asp Lys Glu Glu Gln Ile
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 Phe Leu Val Leu Lys Asp Lys Pro Leu Ser Ser Ile Lys Ala Asp Ile
 610 615 620
 Val His Ala Phe Leu Ser Ile Pro Ser Leu Ser His Ser Val Leu Ser
 625 630 635 640
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 Ser Val Gln Ala Leu Ala Asp Glu Lys Asn Gly Ala Gln Thr Arg Pro
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 Ala Gly Ala Pro Pro Arg Ser Leu Gln Pro Pro Gly Arg Pro Asp
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Pro Tyr Arg Leu Glu Lys Thr Leu Gly Lys Gly Gln Thr Gly Leu Val	
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Lys Leu Gly Val His Cys Ile Thr Gly Gln Lys Val Ala Ile Lys Ile	
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Val Asn Arg Glu Lys Leu Ser Glu Ser Val Leu Met Lys Val Glu Arg	
65 70 75 80	
gag atc gcc atc ctg aag ctc atc gaa cac cca cat gtc ctc aag ctc	288
Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro His Val Leu Lys Leu	
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His Asp Val Tyr Glu Asn Lys Tyr Leu Tyr Leu Val Leu Glu His	
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gtc tcg ggg ggt gag cta ttc gac tac ctg gta aag aag ggg aga ctg	384
Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val Lys Lys Gly Arg Leu	
115 120 125	
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Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln Ile Val Ser Ala Leu	
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Asn Leu Leu Asp Glu Lys Asn Asn Ile Arg Ile Ala Asp Phe Gly	
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Ser Pro His Tyr Ala Cys Pro Glu Val Ile Lys Gly Glu Lys Tyr Asp	
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acc cga cgg gcc ttg gag atg gcc cag cac agc cag aga tcc cgt agc Thr Arg Arg Ala Leu Glu Met Ala Gln His Ser Gln Arg Ser Arg Ser 420 425 430	1296
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Gly Gly Thr Pro Leu His Ser Pro Leu His Thr Pro Arg Ala Ser Pro				
acc ggg acc ccc ggg aca aca cca ccc ccc agc ccc ggc ggt ggc gtc	530	535	540	1632
Thr Gly Thr Pro Gly Thr Thr Pro Pro Ser Pro Gly Gly Gly Val				
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Gly Gly Ala Ala Trp Arg Ser Arg Leu Asn Ser Ile Arg Asn Ser Phe				
ctg ggc tcc cct cgc ttt cac cgg cgc aag atg cag gtc cct acc gct	565	570	575	1728
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Glu Glu Met Ser Ser Leu Thr Pro Glu Ser Ser Pro Glu Leu Ala Lys				
cgc tcc tgg ttc ggg aac ttc atc tcc ttg gac aaa gaa gaa caa ata	595	600	605	1824
Arg Ser Trp Phe Gly Asn Phe Ile Ser Leu Asp Lys Glu Glu Gln Ile				
ttc ctc gtg cta aag gac aaa cct ctc agc agc atc aaa gca gac atc	610	615	620	1872
Phe Leu Val Leu Lys Asp Lys Pro Leu Ser Ser Ile Lys Ala Asp Ile				
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Val His Ala Phe Leu Ser Ile Pro Ser Leu Ser His Ser Val Leu Ser				
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Gln Thr Ser Phe Arg Ala Glu Tyr Lys Ala Ser Gly Gly Pro Ser Val				
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Phe Gln Lys Pro Val Arg Phe Gln Val Asp Ile Ser Ser Ser Glu Gly				
cca gag ccc tcc ccc cga cgg gac ggc agc gga ggt ggt ggc atc tac	675	680	685	2064
Pro Glu Pro Ser Pro Arg Arg Asp Gly Ser Gly Gly Gly Ile Tyr				
tcc gtc acc ttc act ctc atc tcc ggt ccc agc cgt cgg ttc aag cga	690	695	700	2112
Ser Val Thr Phe Thr Leu Ile Ser Gly Pro Ser Arg Arg Phe Lys Arg				
gtg gtg gag acc atc cag gca cag ctc ctg agc act cat gac cag ccc	705	710	715	2160
Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr His Asp Gln Pro				
tcc gtg cag gcc ctg gca gac gag aag aac ggg gcc cag acc cgg cct	725	730	735	2208
Ser Val Gln Ala Leu Ala Asp Glu Lys Asn Gly Ala Gln Thr Arg Pro				

gct ggt gcc cca ccc cga agc ctg cag ccc cca ccc ggc cgc cca gac 2256
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 740 745 750

cca gag ctg agc agc tct ccc cgc cga ggc ccc ccc aag gac aag aag 2304
 Pro Glu Leu Ser Ser Pro Arg Arg Gly Pro Pro Lys Asp Lys Lys
 755 760 765

ctc ctg gcc acc aac ggg acc cct ctg ccc 2334
 Leu Ala Thr Asn Gly Thr Pro Leu Pro
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<210> 4
 <211> 13
 <212> PRT
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<220>
 <223> serine/threonine kinase signature motif consensus
 sequence

<221> VARIANT
 <222> 1
 <223> Xaa= Leu, Ile, Val, Met, Phe, Tyr, or Cys

<221> VARIANT
 <222> 2, 4, 8, 9
 <223> Xaa=any amino acids

<221> VARIANT
 <222> 3
 <223> Xaa= His or Tyr

<221> VARIANT
 <222> 6
 <223> Xaa= Leu, Ile, Val, Met, Phe, or Tyr

<221> VARIANT
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<400> 4
 Xaa Xaa Xaa Xaa Asp Xaa Lys Xaa Xaa Asn Xaa Xaa Xaa
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<210> 5
 <211> 278
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Eukaryotic protein kinase domain

<400> 5
 Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
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 Lys Ala Lys His Lys Thr Gly Lys Ile Val Ala Val Lys Ile Leu Lys
 20 25 30

Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys Arg Leu Ser
35 40 45
His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp Thr Asp Asp
50 55 60
His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp Leu Phe Asp
65 70 75 80
Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala Lys Lys Ile
85 90 95
Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser Asn Gly Ile
100 105 110
Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Asn Gly
115 120 125
Thr Val Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Leu Glu Lys Leu
130 135 140
Thr Thr Phe Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile
145 150 155 160
Leu Glu Gly Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly
165 170 175
Val Ile Leu Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala
180 185 190
Asp Leu Pro Ala Phe Thr Gly Asp Glu Val Asp Gln Leu Ile Ile
195 200 205
Phe Val Leu Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile
210 215 220
Asp Pro Leu Glu Glu Leu Phe Arg Ile Lys Lys Arg Arg Leu Pro Leu
225 230 235 240
Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
245 250 255
Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
260 265 270
Leu Asn His Pro Trp Phe
275

<210> 6
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> UBA domain

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Glu Asp Glu Glu Lys Ile Glu Gln Leu Val Glu Met Gly Phe Asp Arg
1 5 10 15
Glu Glu Val Val Lys Ala Leu Arg Ala Thr Asn Gly Asn Gly Val Glu
20 25 30
Arg Ala Ala Glu Trp Leu Leu Ser His
35 40

<210> 7
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> serkin_6 domain

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 Tyr Glu Leu Leu Lys Lys Leu Gly Lys Gly Ala Phe Gly Lys Val Tyr
 1 5 10 15
 Leu Ala Arg Asp Lys Lys Thr Gly Arg Leu Val Ala Ile Lys Val Ile
 20 25 30
 Lys Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys Lys Asp His Pro
 35 40 45
 Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp Asp Lys Leu Tyr Leu
 50 55 60
 Val Met Glu Tyr Cys Glu Gly Asp Leu Gly Asp Leu Phe Asp Leu Leu
 65 70 75 80
 Lys Lys Arg Gly Arg Arg Gly Leu Arg Lys Val Leu Ser Glu Glu Ala
 85 90 95
 Arg Phe Tyr Phe Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser
 100 105 110
 Gln Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
 115 120 125
 Ser His Val Lys Leu Ala Asp Phe Gly Leu Ala Arg Gln Leu Thr Thr
 130 135 140
 Phe Val Gly Thr Pro Glu Tyr Met Ala Pro Glu Val Leu Gly Tyr Gly
 145 150 155 160
 Lys Pro Ala Val Asp Ile Trp Ser Leu Gly Cys Ile Leu Tyr Glu Leu
 165 170 175
 Leu Thr Gly Lys Pro Pro Phe Pro Gln Leu Asp Leu Ile Phe Lys Lys
 180 185 190
 Ile Gly Ser Pro Glu Ala Lys Asp Leu Ile Lys Lys Leu Leu Val Lys
 195 200 205
 Asp Pro Glu Lys Arg Leu Thr Ala Glu Ala Leu Glu Asp Glu Leu Asp
 210 215 220
 Ile Lys Ala His Pro Phe Phe
 225 230

<210> 8
 <211> 280
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> tyrkin_6 domain

<400> 8
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 Lys Gly Thr Leu Lys Ile Glu Val Ala Val Lys Thr Leu Lys Glu Asp
 20 25 30
 Ala Lys Glu Glu Phe Leu Arg Glu Ala Lys Ile Met Lys Lys Leu Gly
 35 40 45
 Gly Lys His Pro Asn Ile Val Lys Leu Leu Gly Val Cys Thr Glu Glu
 50 55 60
 Gly Arg Arg Phe Met Glu Val Glu Pro Leu Met Ile Val Met Glu Tyr
 65 70 75 80
 Met Glu Gly Gly Asp Leu Leu Asp Tyr Leu Arg Lys Asn Arg Pro Lys
 85 90 95
 Leu Ser Leu Ser Asp Leu Leu Ser Phe Ala Leu Gln Ile Ala Lys Gly
 100 105 110
 Met Glu Tyr Leu Glu Ser Lys Asn Phe Val His Arg Asp Leu Ala Ala
 115 120 125
 Arg Asn Cys Leu Val Gly Glu Asn Lys Val Val Lys Ile Ser Asp Phe
 130 135 140

Gly Leu Ser Arg Asp Leu Tyr Asp Asp Asp Lys Lys Gly Glu Ser Lys
145 150 155 160
Asp Tyr Tyr Arg Lys Lys Gly Gly Lys Thr Leu Leu Pro
165 170 175
Ile Arg Trp Met Ala Pro Glu Ser Leu Lys Asp Gly Lys Phe Thr Ser
180 185 190
Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Thr
195 200 205
Leu Gly Glu Gln Pro Tyr Pro Gly Glu Ile Gln Gln Phe Met Ser Asn
210 215 220
Glu Glu Val Leu Glu Tyr Leu Lys Lys Gly Tyr Arg Leu Pro Lys Pro
225 230 235 240
Glu Asn Asp Leu Pro Ile Ser Ser Val Thr Cys Pro Asp Glu Leu Tyr
245 250 255
Asp Leu Met Leu Gln Cys Trp Ala Glu Asp Pro Glu Asp Arg Pro Thr
260 265 270
Phe Ser Glu Leu Val Glu Arg Leu
275 280